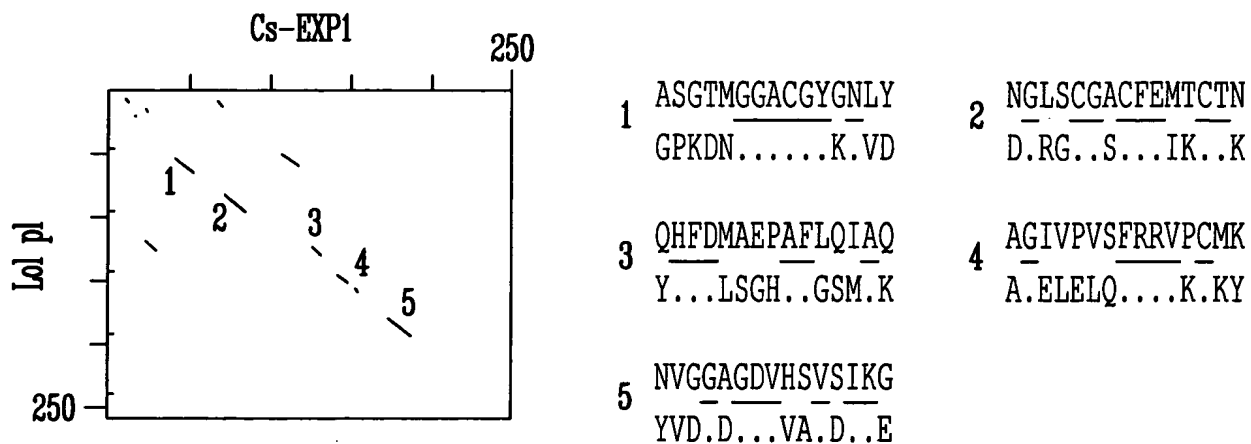
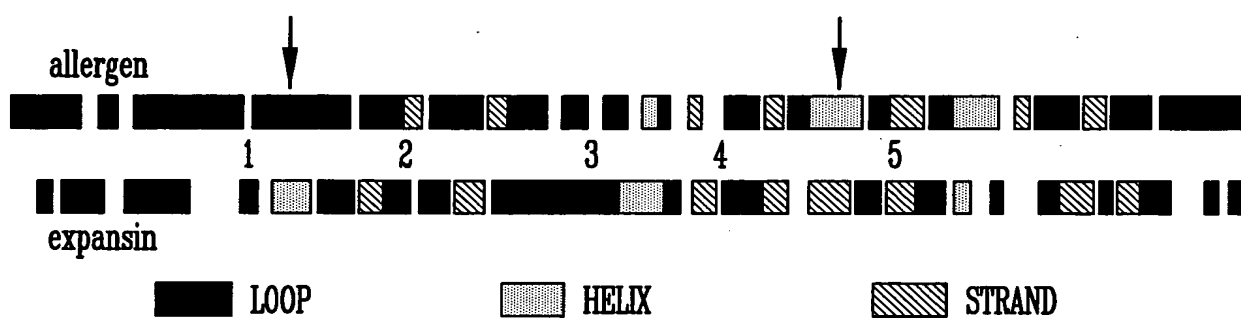


BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
COMPOSITIONS THEREOF AND METHODS OF USE

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*Fig. 1A**Fig. 1B*

BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS, COMPOSITIONS THEREOF AND METHODS OF USE

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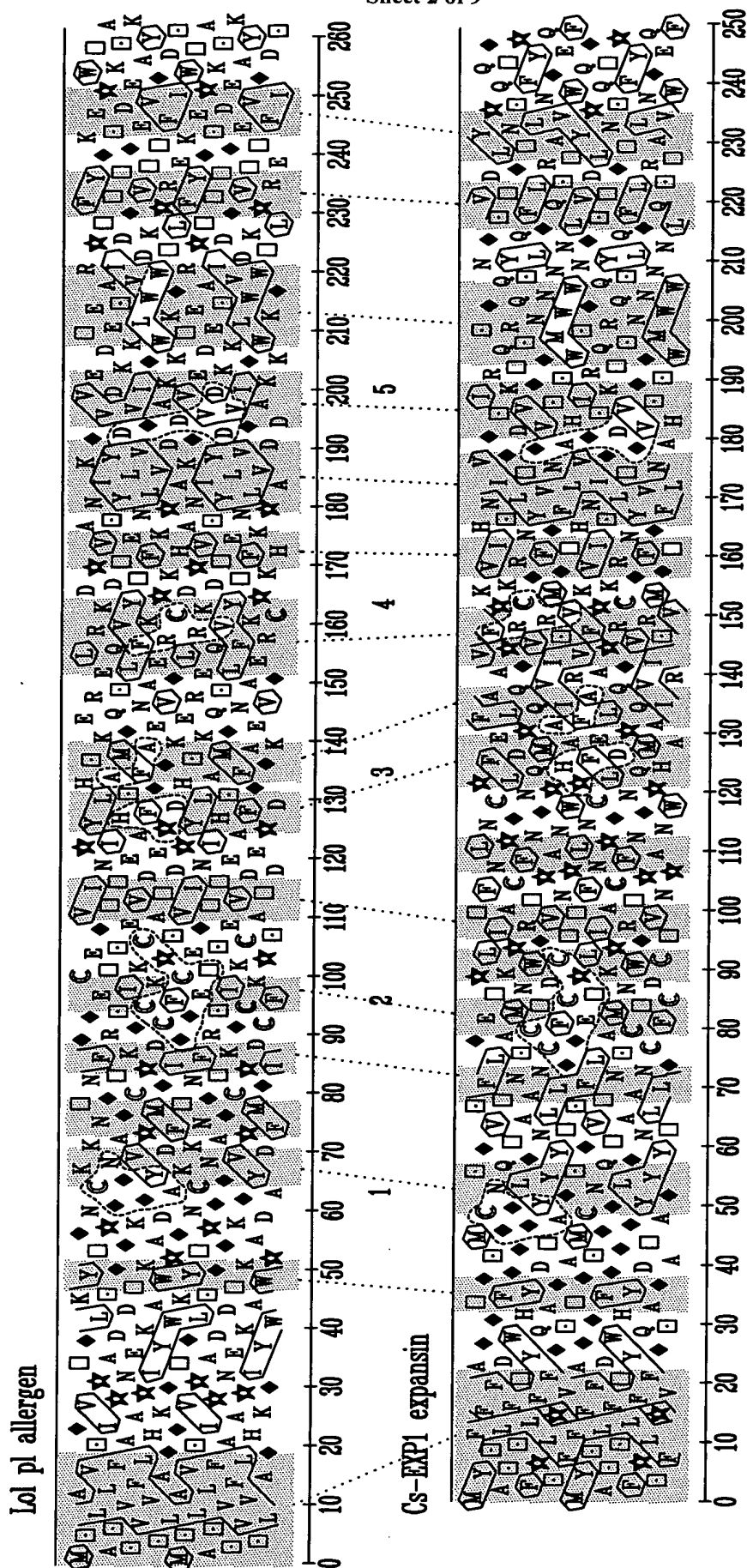


Fig. 1C

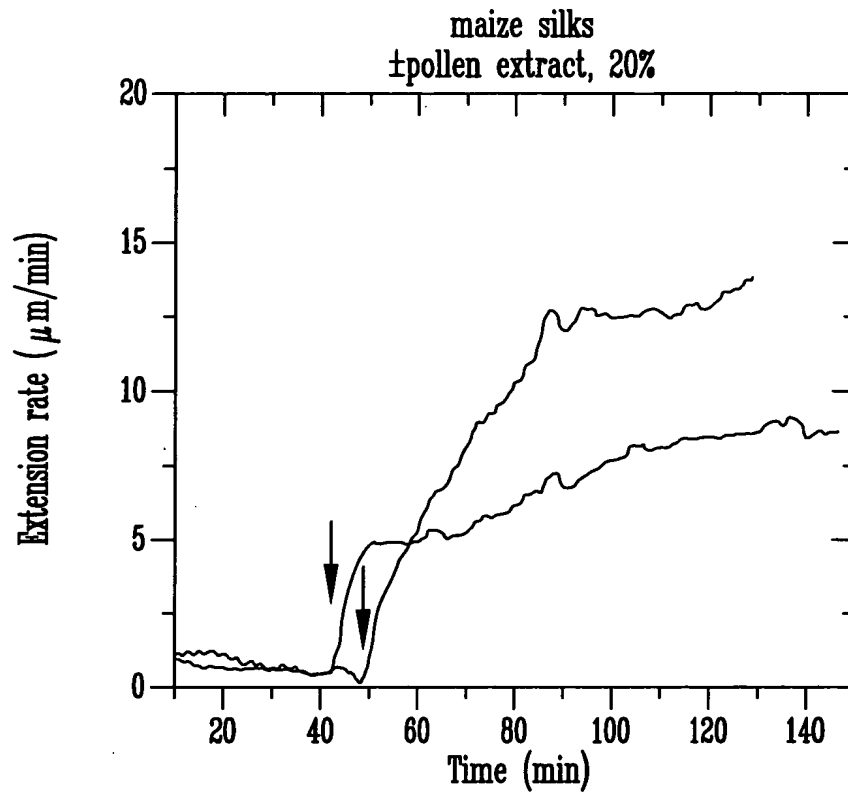


Fig. 2A

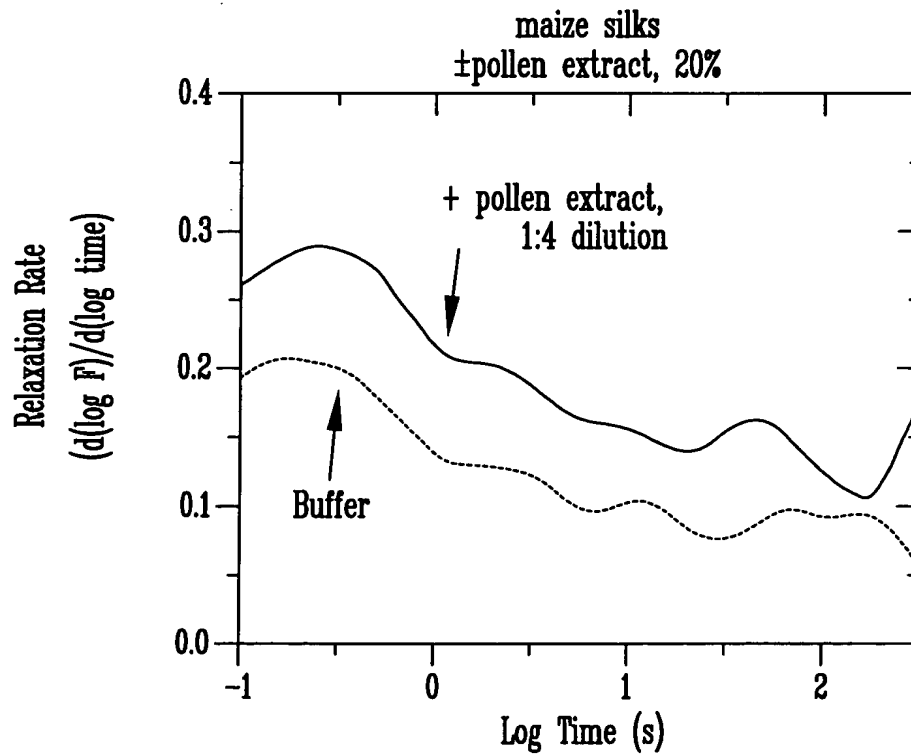
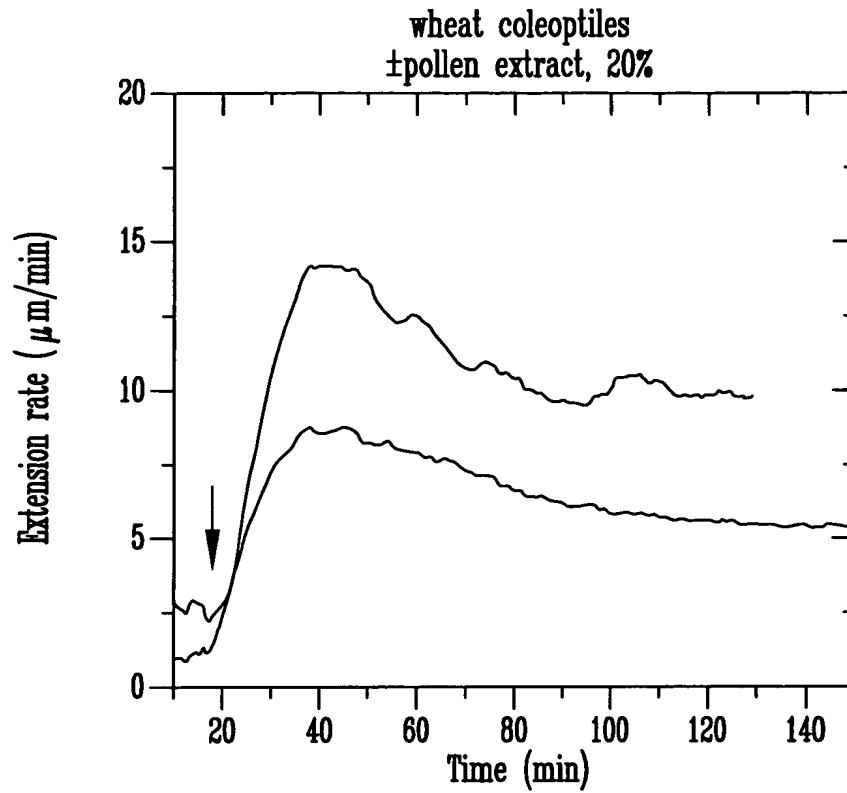
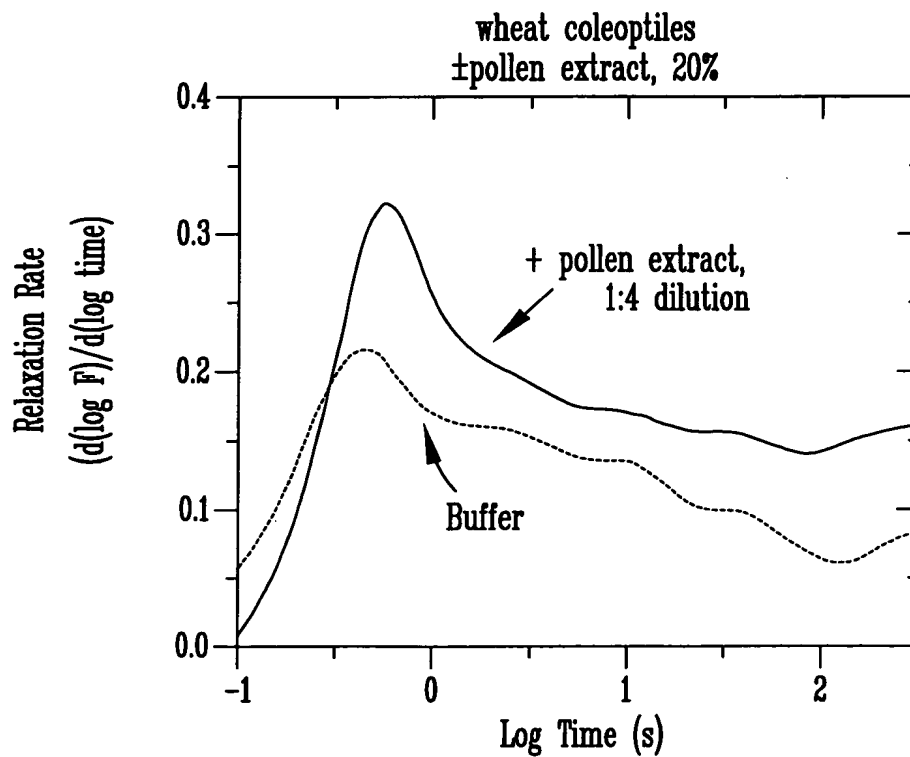


Fig. 2B

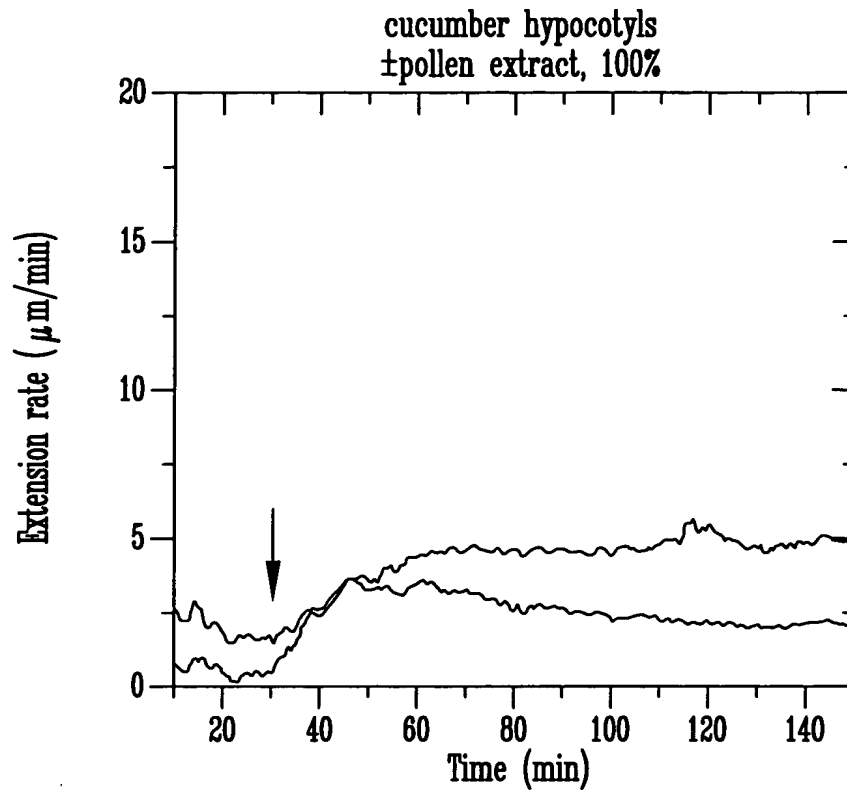
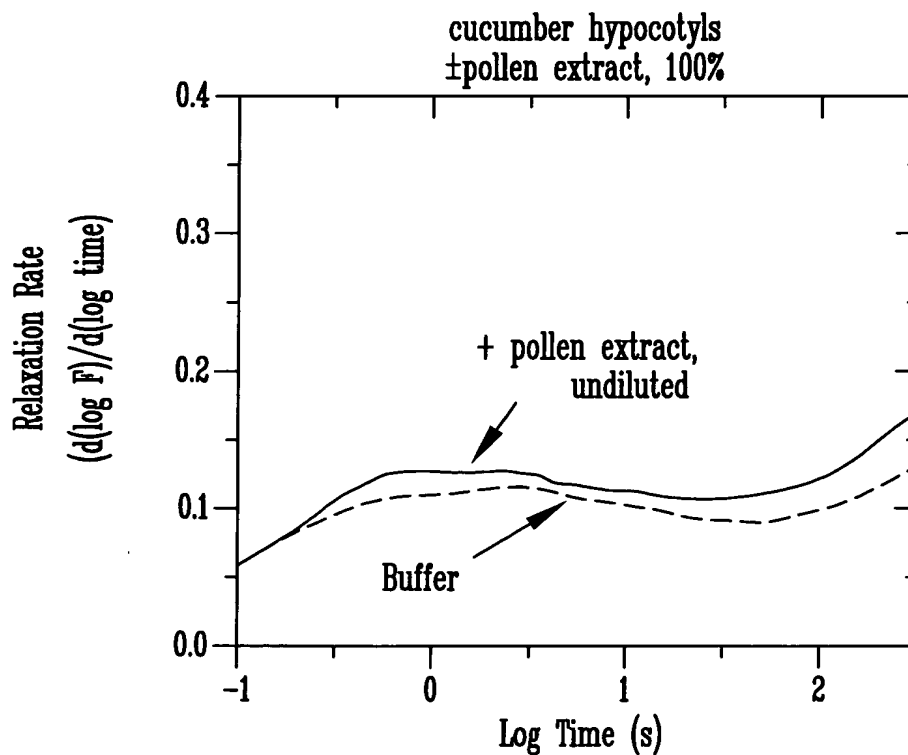
**BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
COMPOSITIONS THEREOF AND METHODS OF USE**

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*Fig. 2C**Fig. 2D*

**BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
COMPOSITIONS THEREOF AND METHODS OF USE**

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*Fig. 2E**Fig. 2F*

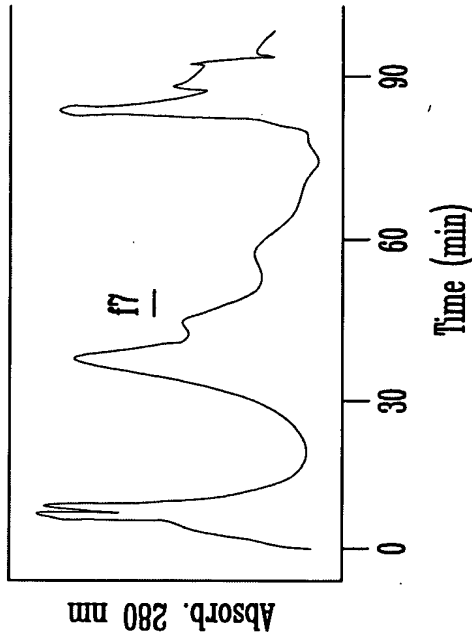


Fig. 3D

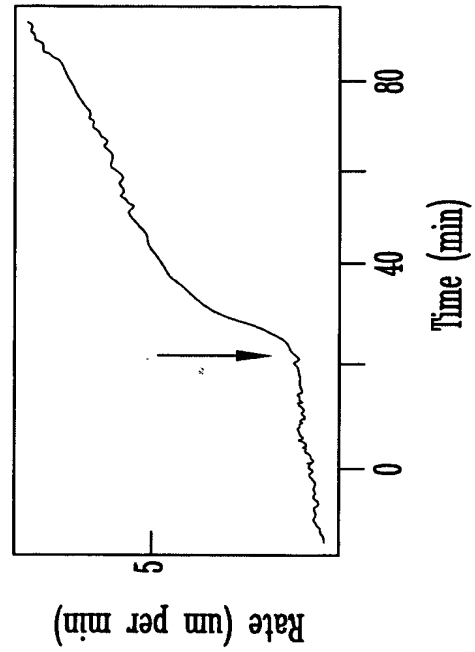


Fig. 3C

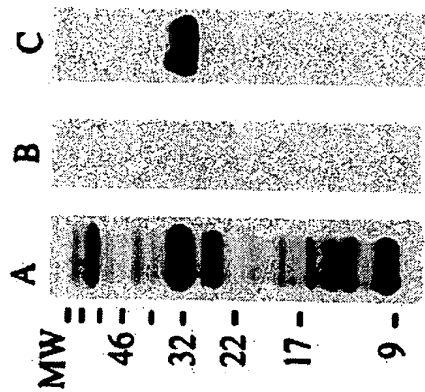


Fig. 3A,B,C

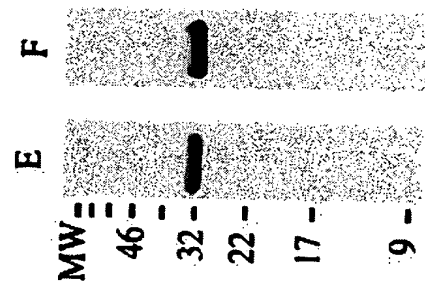


Fig. 3E,F

**BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS,
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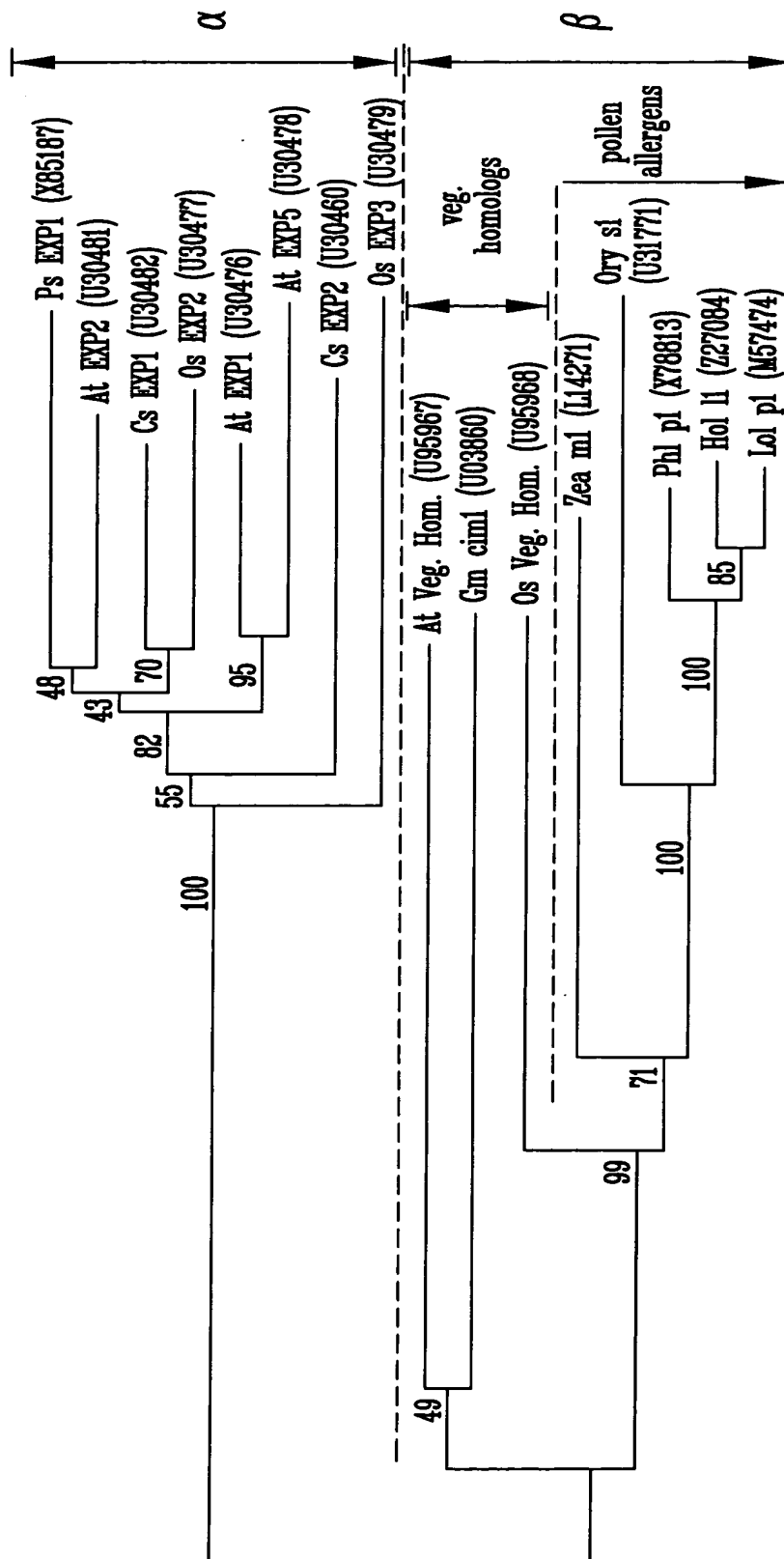


Fig. 4

BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS, COMPOSITIONS THEREOF AND METHODS OF USE

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MASLS---L-LLVAGSL LAV-LG-CFGPTKVL TGSNITVA-ASDWL Majority Consensus #1
 10 20 30 40 50
 1 V-----FLHLLISGS-----GSTPFLTHSNQQVA-ATRW z37641.PRO
 1 MGSLLANNI-----MVGAVLAALVVGSGCPPKVPFGPNITTTNYNGKWL zeamlA.PRO
 1 MASSSSSVL-----LVVA--LFVAVFLGSAHGI AKVPPGPNITABYGDKWL Lolpl.PRO
 1 MAGASAKV-----V--AMLLSVLATYGF AAGVV-----YTNDWL OsEXPlbeta.PRO
 1 MALT LQRALSELLTLIAILSIFLVI PFCFNP KKLYNASY YSPS-SSDW S
 1 MTLVVD RYMYMLHNL L FALTC LLNLN LTHCFSPKK-FNIS AATTS-DSDW S
 1 V-----FLHLLISGS-----GSTPFLTHSNQQVA-ATRW beta2 predicted protein.FRC
 1 ATExPlbeta.PRO
 .A..TWYG...G.G...GGACG...P...G.G Consensus #1
 PATATWYGSPNGAGS--NGGACGYGKNVDQPPFSGMVGAGSPPLFKDGNK Majority
 60 70 80 90 100
 30 PATATWYGSAEGDGS--SGGACGYGSLVDVKPFKARVGA VSPILFKKGGE z37641.PRO
 45 TARATWYGQPNAGAGAPDNGGACGI-KNVNLNLPYSGMTAGC NVPIFKDGK zeamlA.PRO
 43 DAKSTWYGKPTGAGPKDNGGACGY-KNVNDAKPFNGMTGCGNTPIFKDGR Lolpl.PRO
 33 PAKATWYGQPNAGAGPDDNGGACGF-KNTNQYPMFSMTSCGNEPLFQDGK OsEXPlbeta.PRO
 50 FAVATWYGPANGDGS--EGGACGYGNNAVAGQPFSSLSIAGSPLIYDSGK ciml.PRO
 49 IAGSTWYGNPTGYGS--DGGACGYGNNAVAGQPFSSKMVSAGGSPSLFKSGK beta2 predicted protein.FRC
 30 PATATWYGSAEGDGS--SGGACGYGSLVDVKPFKARVGA VSPILFKKGGE ATExPlbeta.PRO
 CG.C....C....CS....TD.....HFDLSG.AFG. Consensus #1
 CGACYEVRCTDKSACSGNPVTVIITDESP--SAKAAHYHFDLSGA AFGA Majority
 110 120 130 140 150
 78 CGACCYKVRCLDKTIICSKRAVTIIATDQSPSGPSAKAKHTHFDLSGA AFGH z37641.PRO
 94 CGSCCYEVRCKEKPECSGNPVTVFITDMM--YEPYAPYHFDLSGKA FGS zeamlA.PRO
 92 CGSCCFEIKCTKPECSGAEAVTVITDNN--EPIAPYHFDLSGHA FGS Lolpl.PRO
 82 CGACCYQIRCTNNPSCSGQPRTVITDHN--YYPVARYHFDLSGTA FGA OsEXPlbeta.PRO
 98 CGSCCYEVKCTGNSACSGNPVKVVITDECAG--CGSDAQYHFDLSGNA FGA ciml.PRO
 97 CGACCYQVKCTSKSACSGKNPVTVFITDECPG--CVKESV-HFDLSGTA FGA beta2 predicted protein.FRC
 78 CGACCYKVRCLDKTIICSKRAVTIIATDQSPSGPSAKAKHTHFDLSGA AFGH ATExPlbeta.PRO
 .A..G....R..G....C.Y....F....L. Consensus #1
 MAIPGLNGVL RNAGLLN LFRRVACKYP-GKNIAFHVEAGSNPNYLA VLV Majority
 160 170 180 190 200
 128 MAIPGLHNGVIRNRGLLNILYRRTACCKYR-GKNIAFHVNAGSTDYWLSL LI z37641.PRO
 140 LAKPGLNDKLRHCGIMDVEFRRVCKCYR-PAGQKIVFHEIEKGCNPNYVAV LV zeamlA.PRO
 138 MAKKGLEQNVRSAGELEQFRRVRCKYR-PDDTKPTFHEVEKASNPNYLA LV Lolpl.PRO
 128 MARPGLNDQLRHAGIIDIQFRRVPC-YHRGLYVNFHVEAGSNPNYLA VLV OsEXPlbeta.PRO
 146 MAISGQDENLRNAGKINIQHRRIECNYP-GRSIAFHVDSGNSQYFAT LV ciml.PRO
 144 MAISGQDSQLRNAGELQILYKKVECNYYI-GKTVTFQVDKGSNANSFAV LV beta2 predicted protein.FRC
 128 MAIPGLHNGVIRNRGLLNILYRRTACCKYR-GKNIAFHVNAGSTDYWLSL LI ATExPlbeta.PRO
 .G....W....WG...W....L..P. Consensus #1
 EYVDGGDGDIGSMEIKEALGSKE---WISMKQSWGAVWRIDVEGPLKGF Majority
 210 220 230 240 250
 177 EYEDGEGDIGSMHIRQA-GSKE---WISMKHIWGANWCI-VEGPLKGF z37641.PRO
 190 KFAVADDGDIVLMEIQDKLSAE---WIKPMKLSWGAIW RMDTAKALKGF zeamlA.PRO
 188 KYVDGDDGTVVAVDIKEKGKDK---WIELKESWGAWWRIDTPDKLTGF Lolpl.PRO
 177 EFANKDGTVVQDLVHESLPSGKPTRVWTPMRRSWSGIWRLDANHRLQGXP OsEXPlbeta.PRO
 195 EYEDGDDGLAKVELKEALDSGS---WDSMQQSWGAVWKKFDKGSPLRAPF ciml.PRO
 193 AYVNGDGEIGRIELKQALDSDK---WLSMSQSWGAVWKKLDVSSPLRAPL beta2 predicted protein.FRC
 177 EYEDGEGDIGSMHIRQA-GSKE---WISMKHIWGANWCI-VEGPLKGF ATExPlbeta.PRO
 SVRLTTLES GKTVIATDVIPANWVPDATYTSNVNF--- Consensus #1
 Majority
 260 270 280 290
 221 SVKLTTLTSSNNKTL SATDVIPSNWVPKATYTSRLNFSPLV z37641.PRO
 235 SIRLTS-ESGKKVIAKDIIPANWRPDAVYTSNVQFY zeamlA.PRO
 233 TVRYTT-EGGKTSEFEDVIEPGWKADTSYSAK Lolpl.PRO
 227 SLRMVS-ESGQTVIAHQV IIPANWRANTNYGSKVQFR OsEXPlbeta.PRO
 241 SIKLTTL ciml.PRO
 239 SLRVTLSLESGKT VVASNVIPANWQPGA IYKSNVNF beta2 predicted protein.FRC
 221 SVKLTTLTSSNNKTL SATDVIPSNWVPKATYTSRLNFSPLV-L ATExPlbeta.PRO

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #1' exactly.

Fig. 5

BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS, COMPOSITIONS THEREOF AND METHODS OF USE

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MAGSSA--VAPLLALLAAAPTGSAXA-----A-YTA-SGWLP Majority
 10 20 30 40 50
 1 HASSSS--VLLVVALFAVFLGSAHGIAK--VPPGPNITAEYGD--KWL D Lol1.PRO
 1 MAGASAK-VYAML LSVLATY-GFAAGVV-----YTN--DWL F OsEXF1beta.PRO
 1 HTILVVD-RVYMLMNL LFPALTCLLLNLTHCFSPKKFNISAATTSDSDW S I beta2 predicted protein.PRC
 1 V-----FLHLLISGSGSTPPLTH-----SNQQVAATR W L F AtEXF1beta.PRO
 1 MAFSYSPFSSLLFLPPFVFT-----FADY--GGW Q S CuEXF1SIGN.PRO
 1 ME--KLFFAFAPFLALSNFFFLPVNA-----FTA-SGW A P CuEXF2sign.PRO
 1 MAGSSAATSCARFLALLATCLLWNEA-----ASPTA-SGW N K OsEXF1.PRO
 1 HALV-----TFLIATLGAMTSNNSA-----RDVNGYAG-GW V N AtEXF1.PRO
 . . . T . Y G G G G A C G F . G . . C Consensus #2
 AHATFYGGPDGSGT M--GGACGCGYGNLYSQGPPFGTNTAALSTALFNDGAG C Majority
 60 70 80 90 100
 44 AKSTWY G K P T G A G P K D N G G A C G Y K N - V D K A P F N G M T G C G N T P I F K D G R G C Lol1.PRO
 34 AKATWY G Q P N G A G P D D N G G A C G F K N - T N Q Y P F M S M T S C G N E P L F D G K G K G C OsEXF1beta.PRO
 50 AGSTWY G N P T G D G S - - D G G A C G Y G N A V A Q P P F S K M V S A G G P S L F K S G K G C beta2 predicted protein.PRC
 31 ATATWY G S A E G D G S - - G G A C G Y G S L V D V K P F K A R V G A V S P I L F K G G E G C AtEXF1beta.PRO
 31 GHATFY G G G D A S G T M - - G G A C G Y G N L Y S Q G - Y G T N T V A L S T A L F N N G L S C CuEXF1SIGN.PRO
 33 AHATFY G E S D A S G T M - - G G A C G Y G N L Y Q T G - Y G T R T A A L S T A L F N D G A S C CuEXF2sign.PRO
 37 AFATFY G G S D A S G T M - - G G A C G Y G D L Y S T G - Y G T N T A A L S T V L F N D G A S C OsEXF1.PRO
 34 AHA F Y G G G D A S G T M - - G G A C G Y G N L Y S Q G - Y G T N T A A L S T A L F N N G L S C AtEXF1.PRO
 G . C C T Consensus #2
 GACFEIRC--TDPKWC--SGTAVTVTATDFCFPHYALPN--GGWCNPP L Q Majority
 110 120 130 140 150
 93 GACFEIKRC--TKRPS C-SGEAVTVTITDDN---EEP-----IAFY Lol1.PRO
 93 GACYQIRK--TNMPS C-SGQPRVTIITDMN---YFP-----VARY OsEXF1beta.PRO
 98 GACYQVKC--TSKSA C-SKNPVTIITDECPGCVKES-----V- beta2 predicted protein.PRC
 79 GACYKVRK--LDKTI C-SKRAVTIATDQSPSGPSAK-----AKHT AtEXF1beta.PRO
 78 GACFEMTC--TNDPKWC L P G T - I R V T A T N F C P P N A L P N N G G W C N P P L K CuEXF1SIGN.PRO
 80 GQC F K I I C D Y K T D P R W C I K G A S V T I T A T N F C P P N A L P N N G G W C N P P L K CuEXF2sign.PRO
 84 G C Y R I M C D Y Q A D R R F C I S G T S V T I T A T N L C P P N A L P N D A G G W C N P P R Q OsEXF1.PRO
 81 G A C F E I R C - - Q N D G K W C L P G S - I V V T A T N F C P P N A L P N N A G G W C N P P Q Q AtEXF1.PRO
 H F D G C F Consensus #2
 HF D L S G P A F G A I A I Y G - - - - - R R A G I V P V L Y R R V F C K Y R G G - - V R F T V N - Majority
 160 170 180 190 200
 127 HFDLSGHAFGSMARKKEEQNVRSAGLELELQFRRVKCYKFD DTKFTPHVER Lol1.PRO
 117 HFDLSGTAFGAMARFGLNDQLRHAGLEIIDIQFRRVPCY-YHRGLYVNFHVEA OsEXF1beta.PRO
 133 HFDLSGTAFGAMAIISGDSQLNRHAGELQILYKKVECHY-IKGTVTQVVDK beta2 predicted protein.PRC
 117 HFDLSGAAPFGHMAIPGHNVIIRNAGLLNILYRRATCKY-RGKNIAFHVHA AtEXF1beta.PRO
 125 HFDMAEPAGLHIAQYIY-- --RA G I V P V S F R R V C H K K G G - - V R F T I W - CuEXF1SIGN.PRO
 130 HFDMAQPAWQKIGIYIY-- --R G I I P V L Y Q R V P C K K R G G - - V R F T V N - CuEXF2sign.PRO
 134 HFDMAEPALWKIGVIYIY-- --R G I V P V M Y Q R V P C A K Q G G - - V R F T I N - OsEXF1.PRO
 128 HFDLSQFVFRORIAQYIY-- --R A G I V P V M Y R R V P C V R R G G - - I R F T I N - AtEXF1.PRO
 L G W W G . . . W Consensus #2
 -GNDYFLLVLVTHVGGAGDVGSVSIK-----GSRTG-WISM SRNWGANW- Majority
 210 220 230 240 250
 177 ASNPNYLA I L V K Y V D G D G D V V A V D I R E - - - - - K G D K W I E L K E S W G A V W R Lol1.PRO
 166 GSNPVYLA I L V E F A N K D G T V V Q L D V M E S L P S G K P T R V W T F M R R S W G S I W R OsEXF1beta.PRO
 182 GSNANSPAV I L V A Y V N G D G E I G R I S L R Q A L - - - - - D S D K W L S M S Q S W G A V W K beta2 predicted protein.PRC
 166 GSTDYWLS I L I E Y E D G E G D I G S M H I R Q A - - - - - G S K E W I S M K H I W G A N W C AtEXF1beta.PRO
 165 -GHSYFNLV I L I T N V G G A G D V H S V S I K - - - - - G S R T G - W Q M S R N W G Q N W - CuEXF1SIGN.PRO
 170 -GRDYFBLV I L I T N V G G A G D I K S V S I K - - - - - G S K S S N W T P M S R N W G A N W - CuEXF2sign.PRO
 174 -GRDYFBLV I L I T N V G G A G S I Q S V S I K - - - - - G S R T G - W M A M S R N W G V N W - OsEXF1.PRO
 168 -GHSYFNLV I L I T N V G G A G D V H S A M V K - - - - - G S R T G - W Q A M S R N W G Q N W - AtEXF1.PRO
 L G W W G . . . W Consensus #2
 -QSNYSYLNGQPLSFRTT-SDGQTLVANNVIPANWQFGQTYSSKVVQFS- Majority
 260 270 280 290 300
 222 IDTPDKL I T G - P F T V R Y T T - E G G T R K S E P R D V I P E G W K A D T S Y S A R Lol1.PRO
 216 LDANHR L I Q G - P X S L R M V S - E S G Q T V I A H Q V I P A N W R A N T N Y G S K V Q F R OsEXF1beta.PRO
 228 LDVS S P L L R A - P L S L R V T S L E S G K T V V A S N V I P A N W Q P G A I Y K S N V N F beta2 predicted protein.PRC
 211 I - V E G P L K G - P F S V K L T T L S N K T L S A T D V I P S N W V P K A T Y T S R L N F S P V AtEXF1beta.PRO
 207 -QSNNYL I N G Q L S F Q V T L - S D G R T L T A Y N L V P S N W Q F G Q T Y E G P - Q F CuEXF1SIGN.PRO
 213 -QSNYSYL I N G Q S L S F K V T T - S D G Q T V Q V F N N V P S S W R F G Q T F A S K V Q F S CuEXF2sign.PRO
 216 -QSNAYL I N G Q S L S F K V T S - S D G Q T L T F L D V A P A G W T F G Q T F T S Q Q F S OsEXF1.PRO
 210 -QSNYSYL I N G Q S L S F K V T T - S D G Q T I V S N N V A N A G W S F G Q T F T G A - Q L R AtEXF1.PRO
 Consensus #2
 Majority
 Lol1.PRO
 OsEXF1beta.PRO
 beta2 predicted protein.PRC
 AtEXF1beta.PRO
 CuEXF1SIGN.PRO
 CuEXF2sign.PRO
 OsEXF1.PRO
 AtEXF1.PRO

Consensus 'Consensus #2': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Fig. 6